

1/10

ATGGCTTTGG	AACAGAACCA	GTCAACAGAT	TATTATTATG	AGGAAAATGA	50
M A L E	Q N Q	S T D	Y Y Y E	E N E	
AATGAATGGC	ACTTATGACT	ACAGTCAATA	TGAACTGATC	TGTATCAAAG	100
M N G	T Y D Y	S Q Y	E L I	C I K E	
AAGATGTCAG	AGAATTTGCA	AAAGTTTTCC	TCCCTGTATT	CCTCACAATA	150
D V R	E F A	K V F L	P V F	L T I	
GTTTTCGTCA	TTGGACTTGC	AGGCAATTCC	ATGGTAGTGG	CAATTTATGC	200
V F V I	G L A	G N S	M V V A	I Y A	
CTATTACAAG	AAACAGAGAA	CCAAAACAGA	TGTGTACATC	CTGAATTTGG	250
Y Y K	K Q R T	K T D	V Y I	L N L A	
CTGTAGCAGA	TTTACTCCTT	CTATTCACCTC	TGCCTTTTTG	GGCTGTTAAT	300
V A D	L L L	L F T L	P F W	A V N	
GCAGTTCATG	GGTGGGTTTT	AGGGAAAATA	ATGTGCAAAA	TAACTTCAGC	350
A V H G	W V L	G K I	M C K I	T S A	
CTTGATACACA	CTAAACTTTG	TCTCTGGAAT	GCAGTTTCTG	GCTTGTATCA	400
L Y T	L N F V	S G M	Q F L	A C I S	
GCATAGACAG	ATATGTGGCA	GTAATAAAG	TCCCCAGCCA	ATCAGGAGTG	450
I D R	Y V A	V T K V	P S Q	S G V	
GGAAAACCAT	GCTGGATCAT	CTGTTTCTGT	GTCTGGATGG	CTGCCATCTT	500
G K P C	W I I	C F C	V W M A	A I L	
GCTGAGCATA	CCCCAGCTGG	TTTTTTATAC	AGTAAATGAC	AATGCTAGGT	550
L S I	P Q L V	F Y T	V N D	N A R C	
GCATTCCCAT	TTTCCCCCGC	TACCTAGGAA	CATCAATGAA	AGCATTGATT	600
I P I	F P R	Y L G T	S M K	A L I	
CAAATGCTAG	AGATCTGCAT	TGGATTTGTA	GTACCCTTTC	TTATTATGGG	650
Q M L E	I C I	G F V	V P F L	I M G	
GGTGTGCTAC	TTTATCACAG	CAAGGACACT	CATGAAGATG	CCAAACATTA	700
V C Y	F I T A	R T L	M K M	P N I K	
AAATATCTCG	ACCCCTAAAA	GTTCTGCTCA	CAGTCGTTAT	AGTTTTTCATT	750
I S R	P L K	V L L T	V V I	V F I	
GTCACTCAAC	TGCCTTATAA	CATTGTCAAG	TTCTGCCGAG	CCATAGACAT	800
V T Q L	P Y N	I V K	F C R A	I D I	
CATCTACTCC	CTGATCACCA	GCTGCAACAT	GAGCAAACGC	ATGGACATCG	850
I Y S	L I T S	C N M	S K R	M D I A	
CCATCCAAGT	CACAGAAAGC	ATCGCACTCT	TTACAGCTG	CCTCAACCCA	900
I Q V	T E S	I A L F	H S C	L N P	
ATCCTTTATG	TTTTTATGGG	AGCATCTTTC	AAAAACTACG	TTATGAAAGT	950
I L Y V	F M G	A S F	K N Y V	M K V	
GGCCAAGAAA	TATGGGTCCT	GGAGAAGACA	GAGACAAAGT	GTGGAGGAGT	1000
A K K	Y G S W	R R Q	R Q S	V E E F	
TTCCTTTTGA	TTCTGAGGGT	CCTACAGAGC	CAACCAGTAC	TTTTAGCATT	1050
P F D	S E G	P T E P	T S T	F S I	
TAAAGGTAAG	ACTGCTCTGC	CTTTTGCTTG	GATACATATG	AATGATGCTT	1100
- R - N	C S A	F C L	D T Y E	- C F	
TCCCCTCAAA	TAAAACATCT	GCCTTATTCT	GAAAAAAM	AAAAAAM	1147
P L K	- N I C	L I L	K K K	K K	

FIG. 1

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CCX-CKR MALEQNQSTDYYYE--ENEMNGTY-----DYSQYELIQIK 33
CCR9 MTPDFTSPIPNMADDYG-SESTSSM-EDYVN----FNFTDF--YCEK
CCR7 MDLGKPMKSVLVVALLVIFQVCLCQDEVTDYIGDNTTVDYTLFESLQSK
CCR6 MSGESMNFSDVFDSSDYFVS-----VNTSMYS-----VDSEML--LQSL
STRL33 MAEHDYHEDYGFSG-----SF-NDSSQEEHQDF--L---

TM1

CCX-CKR EDVREFAKVFLFVFLTIVFVIGTAGNSMVAIVAYYKKQRTKTDVYLLNL 83
CCR9 NNVRQFASHFLPLLYWLVEIVGALNSLMILVWYCTRVTMTDMFLLNL
CCR7 KIVRNFKAFLFIMYSIICFVGILGNGLVLTITIFKRLKIMTDITVLLNL
CCR6 QEVRFQSRLEFPIAYSILQVFGILGNLVMITFAFVKRARSMTDVTLLNM
STRL33 ----QESKVELECMYLVFVCGIVGNSLMVISIFVHQLQSLTDVFLVNL

TM2

TM3

CCX-CKR AMADLLLEFTLPFWAV-NAVHGWVLCKIMCKITSALYTLNFVSGMOFLAC 132
CCR9 AITADLLEFLVTLFPWAIA-AADQWKFTFMCKVNSMYKMFYSCVLLIMC
CCR7 AMADLLEFLTLFPWAYS-AAKSWVFGVHFCKLIFAIYKMSFFSGMLLLC
CCR6 AITADLLEFLVTLFPWAVSHATGAWVFSNATCKLLKGIYAINFNCGMLLLTC
STRL33 PLADLVFVCTLPFWAYA-GIHEWVFGVMMCKSLLGIYITINEYTSMLLLTC

TM4

CCX-CKR ISIDRYVAVTK-VPSQSGVGKPF---CWIICFCVMMAAILLSIEQLVFTV 178
CCR9 ISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWLAAALCIEILYSQI
CCR7 ISIDRYVAVIQAVSAHRHRARVLLISKLSGVGSAILATVLSIEELLYSDL
CCR6 ISMDRYIAIVQATKSFRLRSRTLPRTKIIQLVWGLSVIISSTFVFNQK
STRL33 ITVDHFIVVVKATKAYNQQAQRMTWGVKVTSLLIWISLLVSLFQIYGNV

TM5

CCX-CKR NDNAR---CPIPFPRY-LGTSMKALIQMLEICIGFVVPFLIMGVCFYITA 224
CCR9 KEESGIAICTMVYPS-DESTKLKSAVLTLLKVILGFFLEFVVMACCYTII
CCR7 QRSSEQAMRCSLIT-EHVEAF-ITIQVQMVGFLVPLLAMSFCYLVII
CCR6 YNTQGSDVCEPKYQTVSEPIRWKLLMLGLLELLFGFFIPLMFMIFCYTFIV
STRL33 FNLDKL-IC--GYH--DEAIS--TVVLATQMTLGEFFLELLTMIVCYSVII

TM6

CCX-CKR RTLMKMPNIKISRELKVLLTVIVFIVTQLPYNIVKFCRAIDIIYSLITS 274
CCR9 HTLIQAKSSKHKALKVTITVLTIVFVLSQFPYNCILLVQTIDAYAMFISN
CCR7 RTLLQARNFERNKAIRKVIIVVVFIVFOLPYNGVLAQTVANFNITSST
CCR6 KTLVQAQNSKRHKAIKRIIAVVLVFLACQIPHNMVLLV-TAANLGKMNR
STRL33 KTLHAGGFQKHRSKLIIFLVMAVELLTOMPFNLKMFIRSTH-----WE

FIG. 2A

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TM7

CCX-CKR	CNMSKRMDIAIQVTESTALFHSCNFIILYVFMGASFKNYVMK-----V 317
CCR9	CAVSTNIDICFQVTQTIAFFHSCNFIILYVFMGERFRDLVKTLKNLGCI
CCR7	CELSKQLNTAYDVTYSLACVRCVNFFLYAFIGVKFRNDIFKLFKDLGCL
CCR6	COSEKLIGYTKIVTEVLAFHSCNFIILYVFMGERFRDLVKTLKNLGCI
STRL33	YYAMTSFHYTIMVTEATAYLRACLNEVLYAFVSLKFRKNFWKLVKDIGCL

CCX-CKR	AKKY--GSWRRQRQSV--EFPFDSEGP--TEPTSTFSI	350
CCR9	SQA-QWVSFTR----REGSLK-LSSMLLETTSGALSL	
CCR7	SQE-QLRQWSS----CRHIRR-SSMSVEAETTTTFSP	
CCR6	RRKYKSSGFSCAGRYSENISRQTSETADNDNASSTFM	
STRL33	P--Y--LGVSHQWKSS--DNSKTFASASHNVEATSMFQL	

FIG. 2A
(CONTINUED)

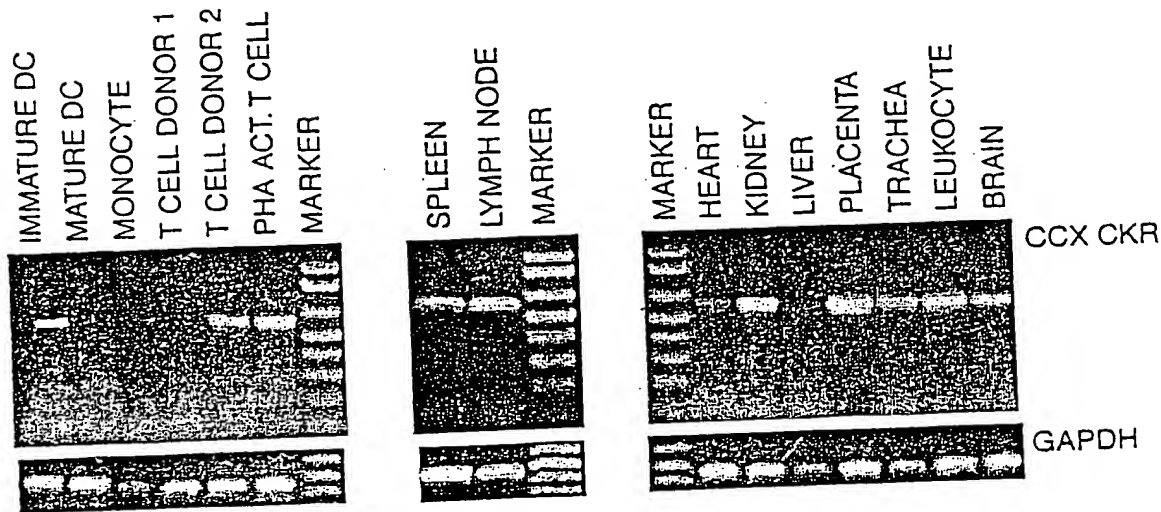


FIG. 2B

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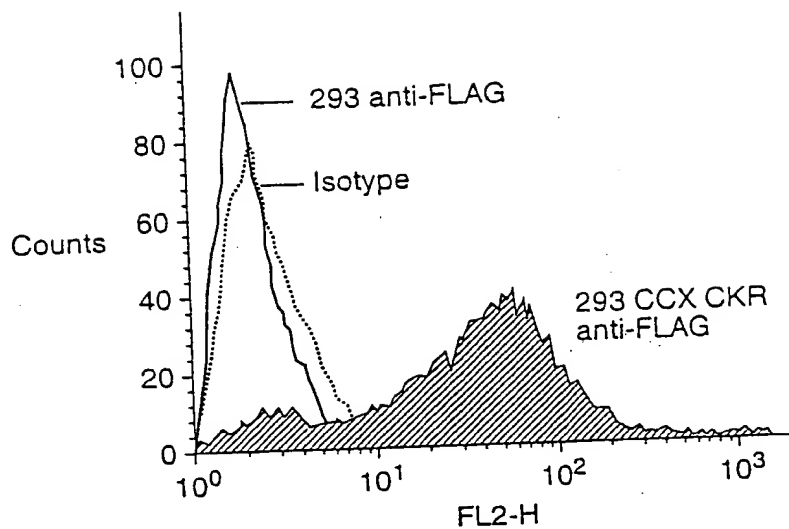


FIG. 2C

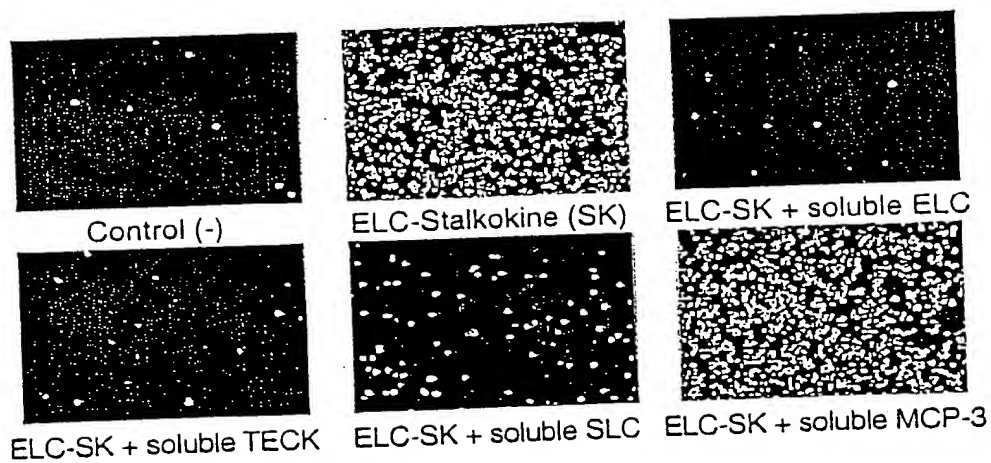


FIG. 3A

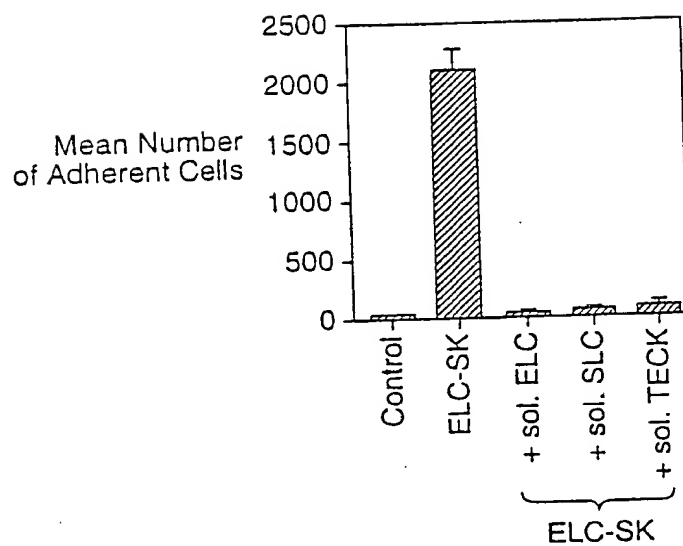


FIG. 3B

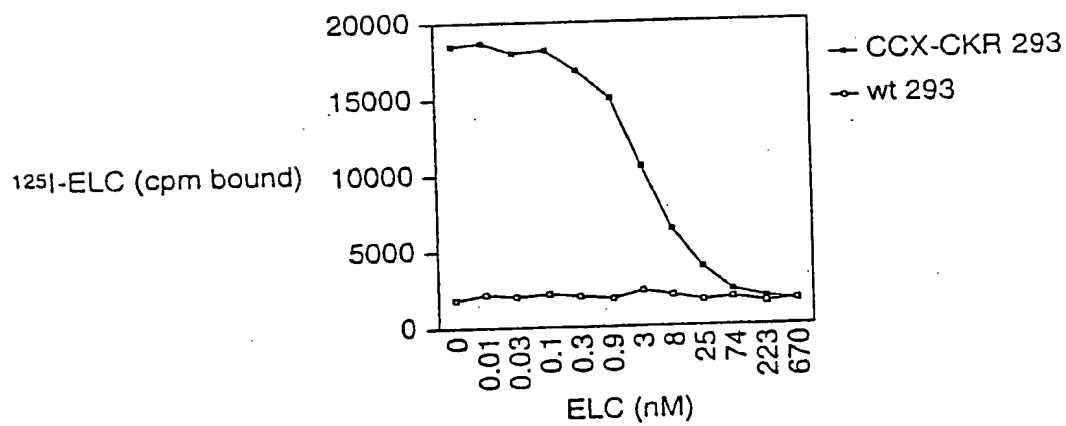


FIG. 3C

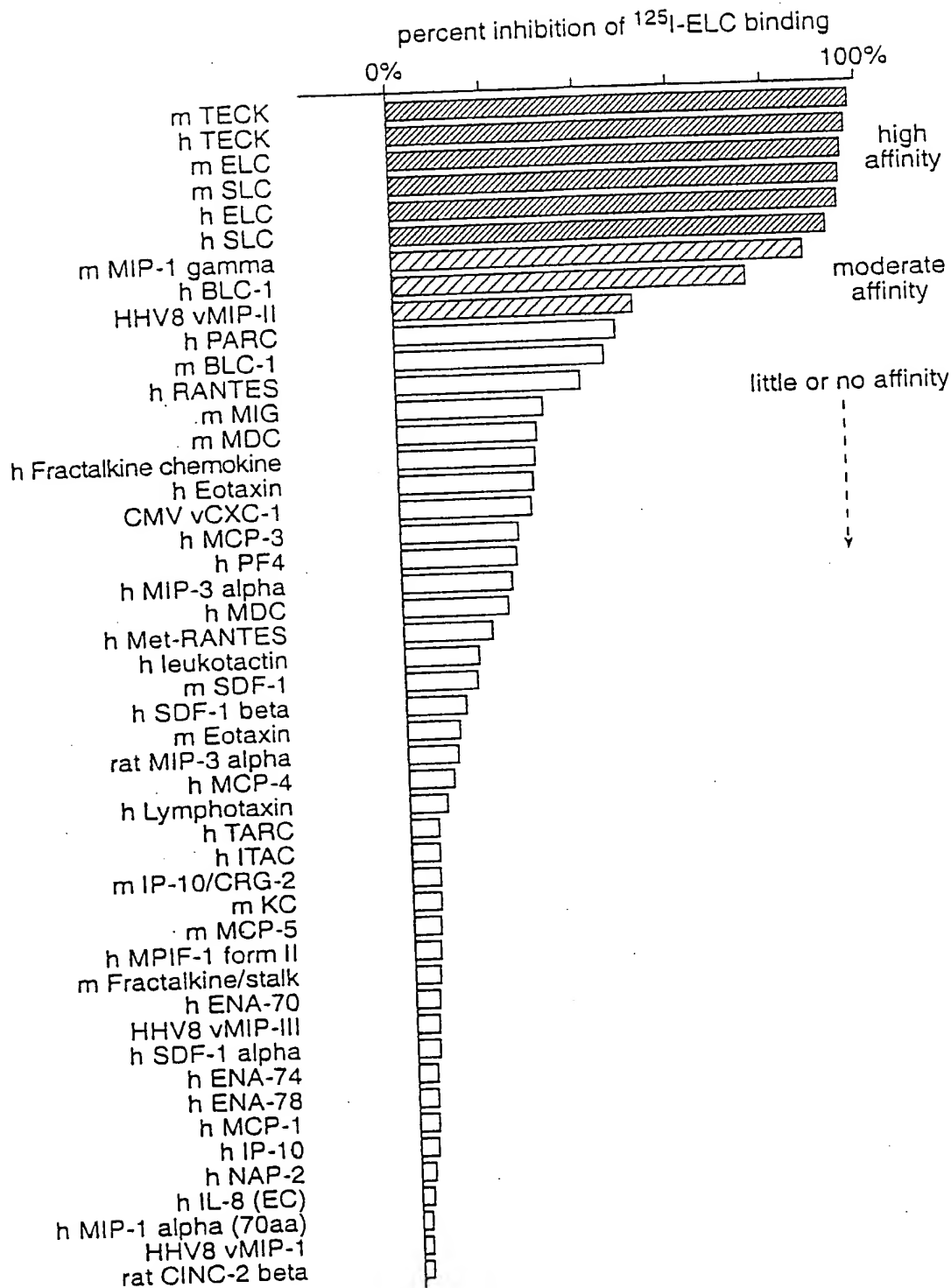


FIG. 4A



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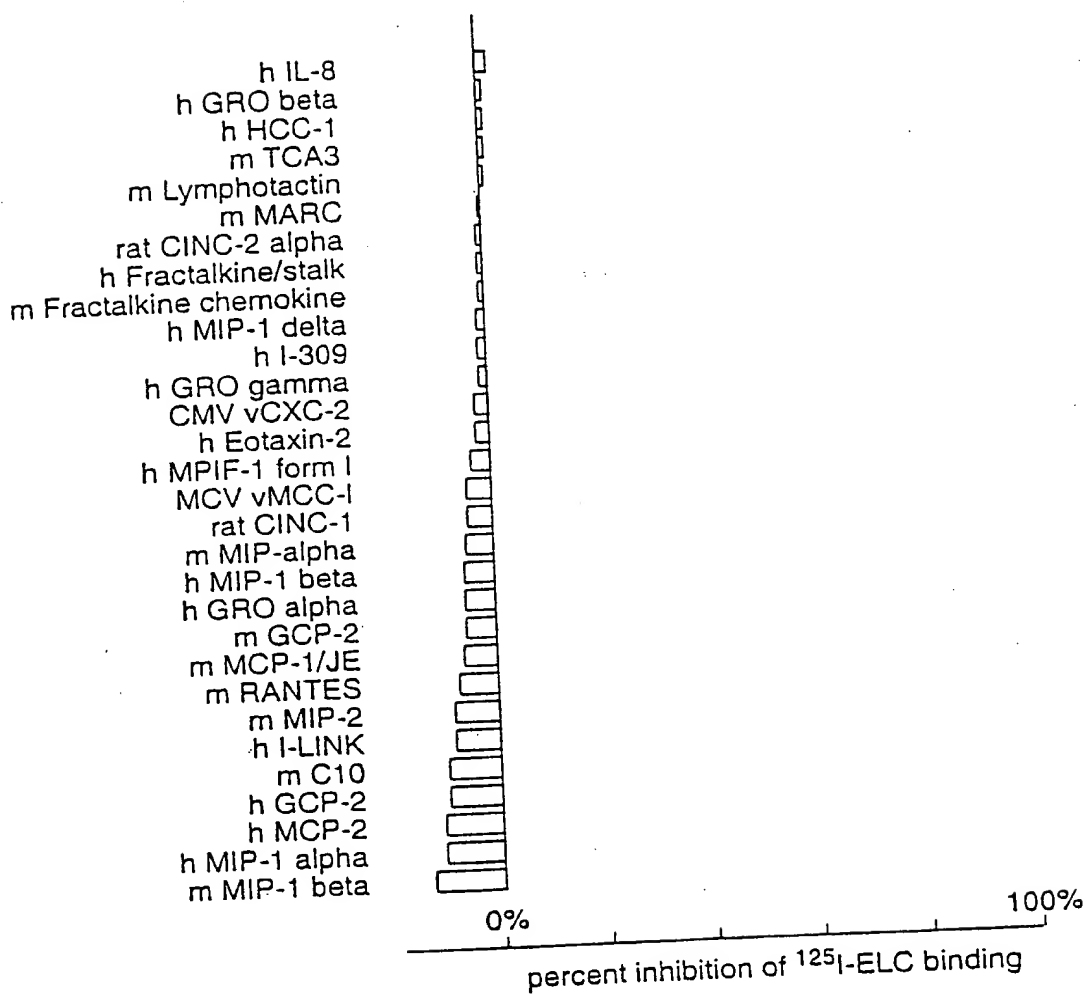
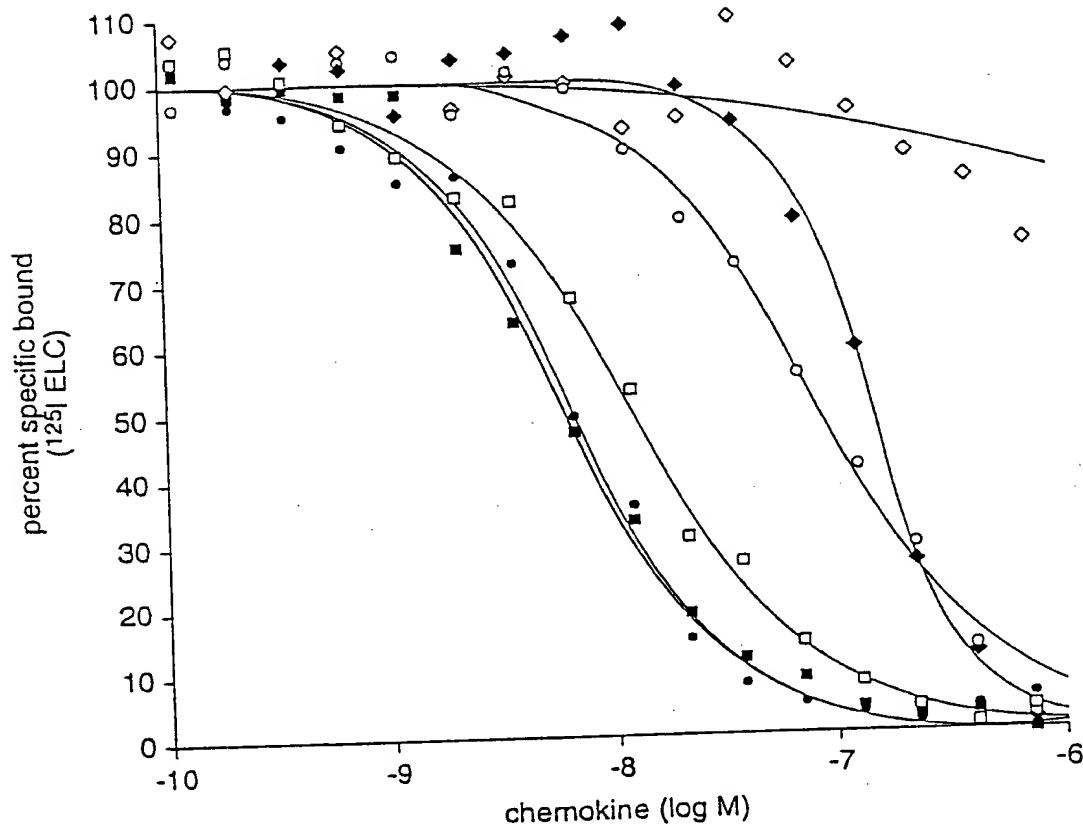


FIG. 4A
(CONTINUED)



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human chemokines		murine chemokines	
	IC-50		IC-50
■ h ELC	6 nM	m ELC	1 nM
□ h SLC	12 nM	m SLC	4 nM
• h TECK	7 nM	m TECK	2 nM
◆ h BLC-1	140 nM	m MIP-1 γ	70 nM
○ HHV8 vMIP-II	90 nM		
◇ h MCP-3	>2000 nM		

FIG. 4B

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5'upstream CCXCKR	ATGCAGCATC	TCGTTTATAA	AAGGCAACTA	GTGAAATTTA	GTGCAAATGC	50	
5'upstream CCXCKR	TGAGAGAATT	TATTTAACTT	ATTTAAATTA	AATTTATAAA	TAACATCAAA	100	
5'upstream CCXCKR	ATAAAAAATA	AATTTAATTT	AAATAAACCA	AGTAATTTGC	TATTTTCGTT	150	
5'upstream CCXCKR	TTTATTCAAT	TTGTTGTAGA	TATACTTTTA	CGATTCACAA	AATTATGTAT	200	
5'upstream CCXCKR	GTAAAGATTA	TAACACTATT	TATTCTTTTT	AGTTAAAATC	TAATTAAATT	250	
5'upstream CCXCKR	TTCATATTTT	AAAAATCATT	TTTACATAAA	AGTCTTCACT	TTTATTTAGG	300	
5'upstream CCXCKR	ATTTAATGAT	TAAGAAAATT	CTCCAGGGCA	TTATGTTTAT	TGTCCTGTTC	350	
5'upstream CCXCKR	AAATCCAAGC	TCTTTCACAC	AGAATTGTAC	AAGCAAAGTT	TGAGTAACTA	400	
5'upstream CCXCKR	ATCTTGGGGT	CATATTCCAA	TGTGGCTCCC	ATTAAAGCAT	TTCAAAGAGT	450	
5'upstream CCXCKR	GCTAGATTCA	GGCTCACATA	TGTTACAGCA	ACAGGCTATA	CTCTAGGGAA	500	
5'upstream CCXCKR	AGAACAAAAC	AGCTTGATAG	AAACTGTGTG	CTTTTAAGCA	TATTTAGACA	550	
5'upstream CCXCKR	AATATCTATC	CTGTATTCTC	TTTGCCATCT	AGATTGGAGC	CATGGCTTTG ATGGCTTTG	600 9	
5'upstream CCXCKR	GAACAGAACC	GTCAACAGA	TTATTATTAT	GAGGAGAGT	GAAATGAATG	649	
	GAACAGAACC	AGTCAACAGA	TTATTATTAT	GAGGA	AAAT	GAAATGAATG	58
5'upstream CCXCKR	GCCTGATGA	CTACAGTCAG	TATGAACTGA	TCTGT	TC	685.	
	GCACTTATGA	CTACAGTCFA	TATGAACTGA	TCTGTATCAA	AGAAGATGTC	108	
5'upstream CCXCKR	AGAGAAAGAGA	CAGAGGATAT	GCACAGGGT	TGCTCCCTGT	ATTGCTCACC	734	
	AGAGAA	TTT	GCAAGAGTTT	TGCTCCCTGT	ATTGCTCACA	147	
5'upstream CCXCKR	ATAG				AG	740	
	ATAGTTTTCG	TCATTGGACT	TGCAGGCAAT	TCCATGGTAG	TGGCAATTTA	197	
5'upstream CCXCKR						740	
	TGCCTATTAC	AAGAAACAGA	GAACCAAAAC	AGATGTGTAC	ATCCTGAATT	247	
5'upstream CCXCKR						740	
	TGGCTGTAGC	AGATTTACTC	CTTCTATTCA	CTCTGCCTTT	TTGGGCTGTT	297	
5'upstream CCXCKR						740	
	AATGCAGTTC	ATGGGTGGGT	TTTAGGGAAA	ATAATGTGCA	AAATAACTTC	347	

FIG. 5

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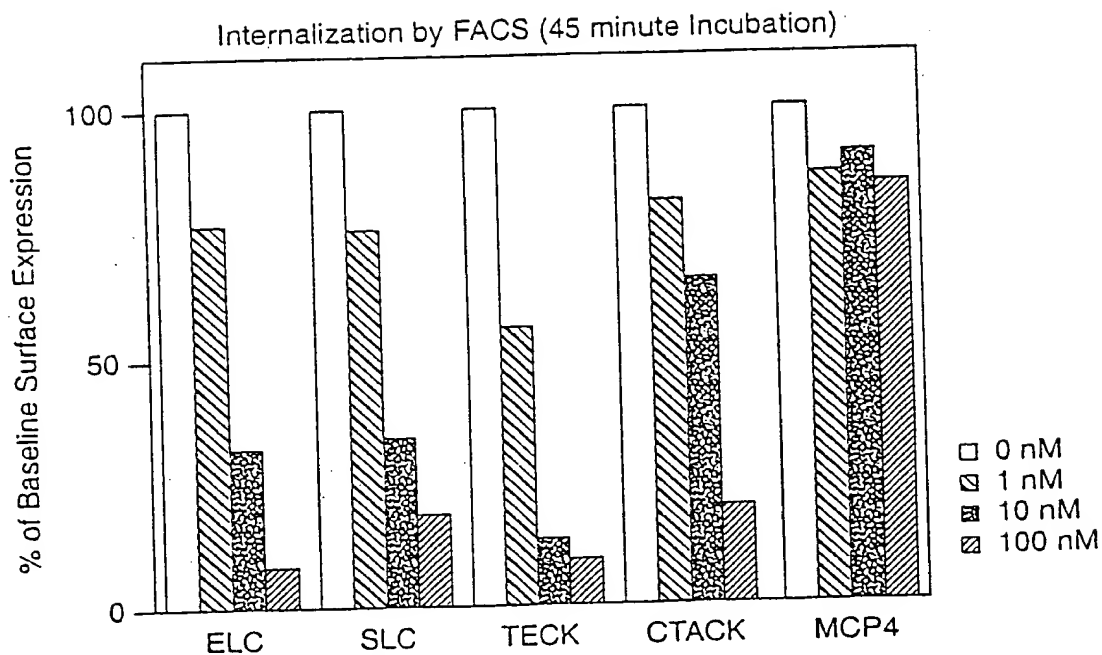


FIG. 6A

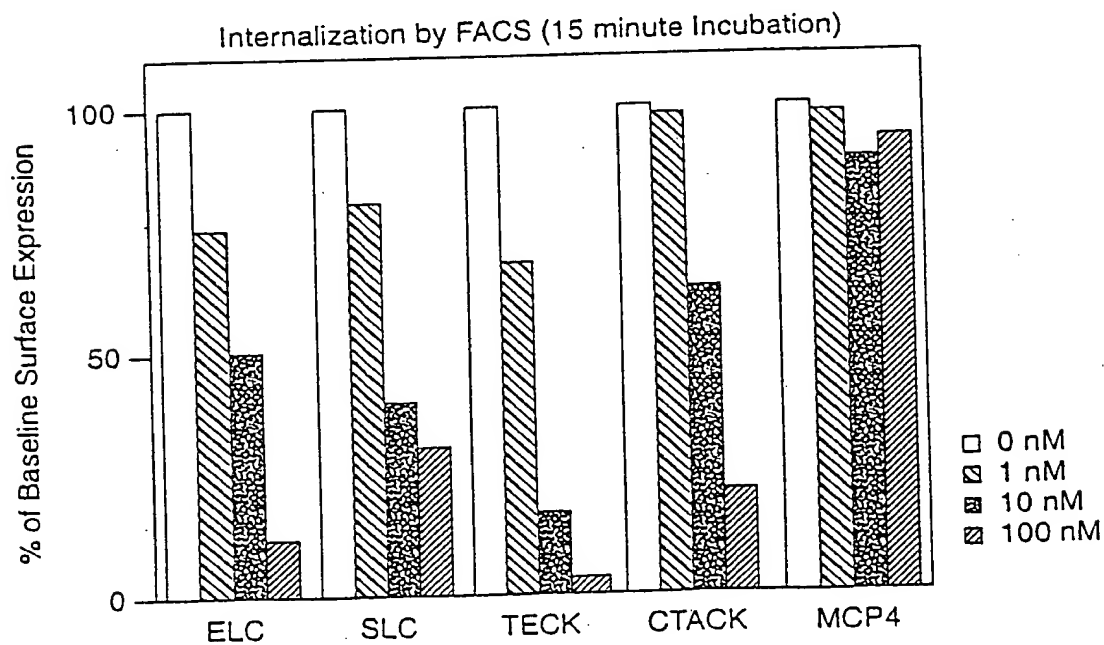


FIG. 6B